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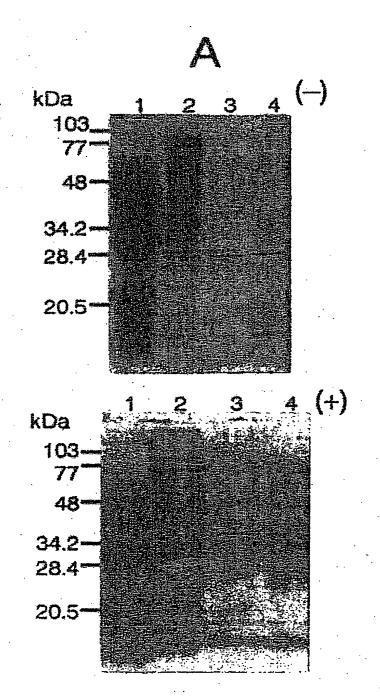
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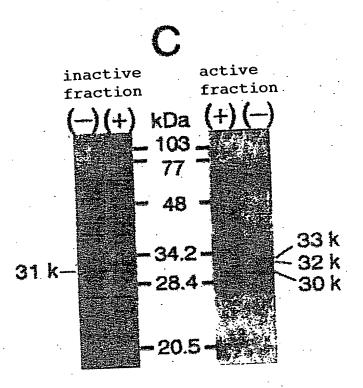
[Figure 1]

[Figure 2]



[Figure 2]

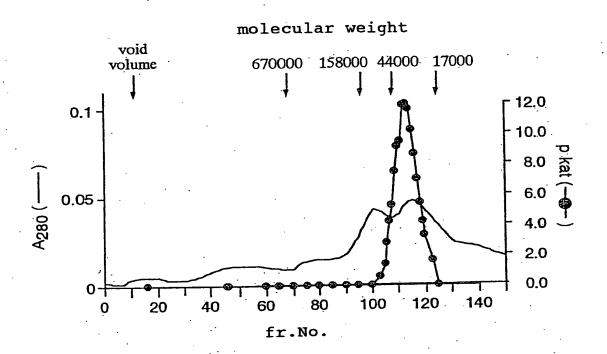
[Figure 2]



[Figure 3]



[Figure 4]



[Figure 5]

DAQNKEVAALIEKIAGIQA :::::::::::::::::::::::::::::::::::	YVNLSKLEYDLLVRYVPGIAPTRVAFVGSGPLPFSSLVLAAHHLPDAVFDNYDRCGAANERARRLFRGÀDEGLGARM~ TF primer AFHTGDVATLTGELGAYDVVFLATLVGMAAEEKP	SFHTADVADLTGELGAYDVVFLAALVDMAAEEKAKVIAHLGAHMVEGASLVVYSAHGARGFLYP SFHTAEVTDLTAELGAYDV 30 kDa -2 ADGAVLVARSAHGARAFLYPVVELDDVGR	
DAGNKEVAALIEKIAGIQA ::::::::::::::::::::::::::::::::::::	YVNLSKLEYDLLVRYVPGIAPTRVAFVGSGPLPFS — IF primer —AFHTGDVATLTGELGAYDVVFLATLVGMAAEEKP	SFHTADVADLTQELGAYDVVFLAALVDMAA	PEDIRRGGFEVLAVHHPEGE
33,32 kDa -1 rice (D24790)	rice (D23792)	33,32 kDa -3 30 kDa -1	33,32 kDa -4

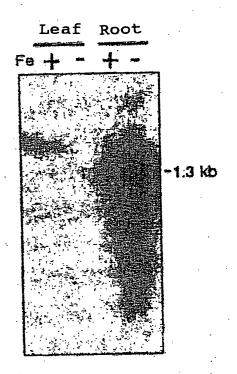
[Figure 6]

	GCG	TTC	AGA	GGÇ	TTC	CAG	AGT	TCT	TCC	GGT	CAC	CAA	gaa	GCA	Ш	GAT	CAT	AAC	54
19		GAT	GCC A'	-	AAC N	AAG K	_	GTC V	GCT A	GCT ·A		ATC I	GAG E	AAG K	ATC I	GCC A	GGT G	ATC I	108
37	. •	~	GCC A	ATC			CTG L	CCG P	TCG S	CTG L	AGC S		TCC S	CCC P	GAG E	GTC V	GAC D	AGG R	162
55		ΠC		GAC D		GTC V	ACG T	GCC	TGC	GTC V	CCG P	CCG P			GTC V	GAC D	GTG V	ACG T	216
73	AAG K	CTC	AGC S	CCG	GAG E	CAC H	CAG Q	AGG R	ATG M		GAG E		CTC	ATC	.CGC R	TTG	TGC	TCC S	270
91	GCC	-	GAG E	-		CTC	GAG		CAC	TAC	GCC	GAC		стс			TTC		.324
109	. •					•				CCG	•	TAC	AGC	AAC		•	AAC N	-	378
	••	-		_		GAG		_	-		-					•	CCG-	GCG A	432
127	CGC	GTC	GÇC	TTC	GTC	GGC	TCC	GGC	CCG	CTG	CCG	ПС	ÁGC	TCG		GTC	ĊŢC		486
145	GCG						ACC							S CŢG		V GGC	GÇG	GÇC	540
163	A AAC	H	H	GCC	P AGG	E AAG	T CTG	. Q TTC	F GGC		N ACG	GCG	D GAC	GGC	. C GTC	G GGC	.GCG	A	594
181	N ATC	E	R	A	R		L	F	G	A	T	ACC	D	. G	V	Ġ	A	R	640
199	M @	S	F	H	T	Å	D	V .	A	D	CTC	T	Q	E	L	G	Å	TAC	648
217	GAC D	GTG V	GTC V	ΠC F	CTC L	GCC A	GCG A	CTC	GTC V		ATG M	GCA A	GCC A	GAG E	GAG E	AAG K	GCC A	AAG K	702
235	GTG V		GCC A	CÁC H	CTG	GGC G	GCG A	CAC H	ATG M	GTG V	GAG E	GGG G	GCG A	TCC S	CTG	GTC V	GTG V	CGG R	756
253	AGC S	GCA A	CGG R	CCC	CGC R	GGC G	TTT F	c [T	TAC Y	CCC	ATT	GTC V	D.	CCG P	GAG E	GAC D	ATC I	ÁGG R	810
271	CGG R	GGT G		TTC F	GAG E	GTG V	CTG	GCC A	GTG V	CAC	CAC H	CCG P		-	GAG E	GTG V	ÁTC	AAC N	864
289	TCT S	GTC V	ATC I	GTC V	GCC A	CGT R		GCC A	GTC V	GAA E	GCG A	CAG Q	CTC	AGT S	GGG	ĊÇG	CAG	AAC'	918
307	GGA G	GAC D	GCG A	CAC	GCA A	CGG R		GCG A	GTG V	CCG P		GTC V	AGC S	CCG	CCA P	TGC	AAC N		972
325	TCC S	ACC T	AAG · K	ATG M	GAG E	GCG A	AGC S	GCG A	CŢŦ	GAG E	AAG K	AGC	GAG F	GAG F	CTG	ACC	GCC A	AAA K	1026
•		CTG	GCC												-		GAT		1080
		_		-	-	CGT	GTG	<u>T</u> GT	Ш	GAT	GTT	ŢĠŢ	GCC	TGT	AAG	AGT	TAT TTA	GCT	1134
	CIG	GAA	IAA	CGG	TAT	GTA	ACA	TAA	ATA	TTA	GTG	GGA	ПТ	GAA	GTG	.TAA	TTA TGC AAA	TAA	1188 1242

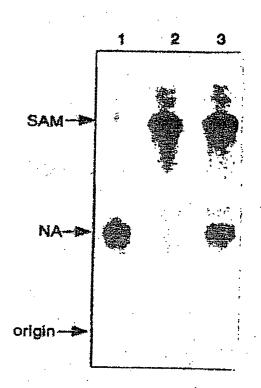
[Figure 7]

NAS 1 NAS 2 NAS 3 NAS 4 NAS 5-1 NAS 5-2 NAS 6	1 MDAQNKEV AALIEKIAGI QAAIAELPSL SPSPEVDRLF TDLYTACVPP 1 MAAQNN-QEV DALVEKITGL HAAIAKLPSL SPSPDVDALF TELYTACVPP 1 MAAQNNNKDV AALVEKITGL HAAIAKLPSL SPSPDVDALF TELYTACVPP 1 MDGQSEEV DALVQKITGL HAAIAKLPSL SPSPDVDALF TDLYTACVPP 1 MEAENGEV AALVEKITGL HAAISKLPAL SPSPQVDALF TELVAACVPS 1 MEAENGEV AALVEKITGL HAAISKLPAL SPSPQVDALF TELVAACVPS 1 MDAQNKEV DALVQKITGL HAAIAKLPSL SPSPDVDALF TDLYTACVPP 2 * ** ** ** ** ** ** ** ** ** ** ** **	0000
NAS 1 NAS 2 NAS 3 NAS 4 NAS 5-1 NAS 5-2 NAS 6	51 SPVDVTKLSP EHQRMREALI RLCSAAEGKL EAHYADLLAT FDNPLDHLGL 51 SPVDVTKLGP EAGEMREGLI RLCSEAEGKL EAHYSDMLAA FDKPLDHLGM 51 SPVDVTKLGP EAGEMREGLI RLCSEAEGKL EAHYSDMLAA FDNPLDHLGI 51 SPVDVTKLAP EAGAMREGLI RLCSEAEGKL EAHYSDMLAA FDNPLDHLGV 51 SPVDVTKLGP EAGEMRQDLI RLCSAAEGLL EAHYSDMLTA LDSPLDHLGR 51 SPVDVTKLGP EAGEMRQDLI RLCSAAEGLL EAHYSDMLTA LDSPLDHLGR 51 SPVDVTKLGS EAGEMREGLI RLCSEAEGKL EAHYSDMLTA LDSPLDHLGR 51 SPVDVTKLGS EAGEMREGLI RLCSEAEGKL EAHYSDMLTA DSPLDHLGM	00000
NAS 1 NAS 2 NAS 3 NAS 4 NAS 5-1 NAS 5-2 NAS 6	101 FPYYSNYVNL SRLEYELLAR HVPG-IAPAR VAFVGSGPLP FSSLVLAAHH 101 FPYYNNYINL SKLEYELLAR YVPGGYRPAR VAFIGSGPLP FSSFVLAARH 101 FPYYSNYINL SKLEYELLAR YVRR-HRPAR VAFIGSGPLP FSSFVLAARH 101 FPYYSNYINL SKLEYELLAR YVPGRHRPAR VAFIGSGPLP FSSFVLAARH 101 FPYYFDNYVNL SKLEHDLLAG HW	0000
NAS 1 NAS 2 NAS 3 NAS 4 NAS 5-1 NAS 5-2 NAS 6	151 LPETGFDNYD LCGAANERAR KLFGATADGV GARMSFHTAD VADLTGELGA 151 LPDTMFDNYD LCGAANDRAS KLFRADRD-V GARMSFHTAD VADLAGELAK 151 LPDTMFDNYD LCGAANDRAS KLFRADTD-V GARMSFHTAD VADLASELAK 151 LPDTVFDNYD LCGAANDRAT RLFRADKD-V GARMSFHTAD VADLTDELAT 151 LPDTRFDNYD RCSVANGRAM KLVGAADEGV RSRMAFHTAE VTDLTAELGA 151 LPDTRFDNYD RCSVANGRAM KLVGAADEGV RSRMAFHTAE VTDLTAELGA 151 LPDAMFDNYD LCSAANDRAS KLFRADKD-V GARMSFHTAD VADLTRELAA 201 151 LPDAMFDNYD LCSAANDRAS KLFRADKD-V GARMSFHTAD VADLTRELAA 201 152 LPDAMFDNYD LCSAANDRAS KLFRADKD-V GARMSFHTAD VADLTRELAA 201 153 LPDAMFDNYD LCSAANDRAS KLFRADKD-V GARMSFHTAD VADLTRELAA 201 201 201 201 201 202 203 203 204 205 205 205 205 205 205 205 205 205 205	0.000
NAS 1 NAS 2 NAS 3 NAS 4 NAS 5-1 NAS 5-2 NAS 6	201 YDVVFLAALV GMAAEEKAKV IAHLGAHMVE GASLVVRSAR P-RGFLYPIV 25- 201 YDVVFLAALV GMAAEDKAKV IAHLGAHMAD GAALVVRSAH GARGFLYPIV 25- 201 YDVVFLAALV GMAAEDKAKV IAHLGAHMAD GAALVVRSAH GARGFLYPIV 25- 201 YDVVFLAALV GMAXEDKAKV IAHLGAHMAD GAALVARSAH GARGFLYPIV 25- 201 YDVVFLAALV GMTSKEKADA IAHLGKHMAD GAVLVARSAH GARAFLYPVV 25- 201 YDVVFLAALV GMTSKEKADA IAHLGKHMAD GAVLVARSAH GARAFLYPVV 25- 201 YDVVFLAALV GMAXEDKAKV IPHLGAHMAD GAVLVARSAH GARAFLYPVV 25- 25- 26- 27- 28- 28- 28- 28- 28- 28- 28- 28- 28- 28	00000
NAS 1 NAS 2 NAS 3 NAS 4 NAS 5-1 NAS 5-2 NAS 6	251 DPEDIRRGGF EVLAVHHPE- GEVINSVIVA RKAVEAQLSG PQNGDA 251 DPQDIGRGGF EVLAVCHPD- DDVVNSVIIA QKSKDVHADG LGSGRGAGGQ 300 251 DPQDIGRGGF EVLAVCHPD- DDVVNSVIIA QKSKEVHADG LGSARGAGRQ 300 251 DPQDIGRGGF EVLAVCHPD- DDVVNSVIIA QKSNDVHEYG LGSGRG-GR- 251 ELDDVGRGGF QVLAVHHPAG DEVFNSFIVA RKVKMSA 251 ELDDVGRGGF QVLAVHHPAG DEVFNSFIVA RKVKMSA 251 DPQDIGRGGF EVLAVCHPD- DDVVNSVIIA HKSKDVHANE RPNGRG-G-Q 300 251 DPQDIGRGGF EVLAVCHPD- DDVVNSVIIA HKSKDVHANE RPNGRG-G-Q 300	0
NAS 1 NAS 2 NAS 3 NAS 4 NAS 5-1 NAS 5-2	301 HARGA-VPLV SPPCNFSTKM EASALEKS EELTAKELAF 301 YARGT-VPVV SPPCRFGE-M VADVTQNHKR DEFANAEVAF 301 YARGT-VPVV SPPCRFGE-M VADVTQNHKR DEFANAEVAF 301 YARGTVVPVV SPPCRFGE-M VADVTQKR EEFANAEVAF	
NAS 6	301 Y-RGA-VPVV SPPCRFGE-M VADVTHKR EEFTNAEVAF (** **** * * * * * * **)	

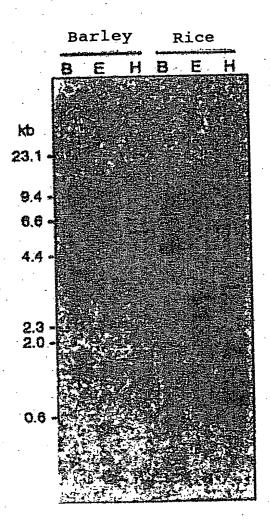
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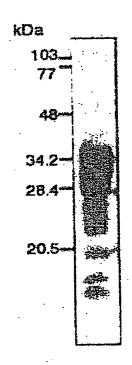
[Figure 8]



[Figure 10]



[Figure 11]



[Figure 12]

